AMENDMENTS TO THE CLAIMS

Please amend claims 29-33, 37, 39-41, 52, 54, and 55, and add new claims 56-76, as set forth below.

Please cancel claims 28, 34-36, and 38.

Please withdraw claims 1-27 and 43-51, without prejudice or disclaimer.

The current listing of claims replaces all prior listings.

1. (Withdrawn) A method to infer breed of a bovine subject from a nucleic acid sample of the bovine subject, comprising identifying in the nucleic acid sample, at least one nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the SNP is associated with a breed, thereby inferring the breed of the bovine subject.

2. (Withdrawn) The method of claim 1, wherein the nucleotide occurrence of at least 2 of the SNPs is determined to infer the breed.

3. (Withdrawn) The method of claim 2, wherein the nucleotide occurrences of the at least 2 SNPs comprise a haplotype allele, and wherein the method infers the breed using the identified haplotype allele.

4. (Withdrawn) The method of claim 3, further comprising identifying a diploid pair of haplotype alleles and inferring the breed using the diploid pair of haplotype alleles.

5. (Withdrawn) The method of claim 1, wherein the identified nucleotide occurrence is associated with Angus, Holstein, Limousin, Brahman, Simmental, Hereford, Gelbvieh or Charolais cattle.

6. (Withdrawn) The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Angus cattle is identified.

7. (Withdrawn) The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Brahman cattle is identified.

8. (Withdrawn) The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Limousin cattle is identified.

9. (Withdrawn) The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Simmental cattle is identified.

10. (Withdrawn) The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Hereford cattle is identified.

11. (Withdrawn) The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Charolais cattle is identified.

12. (Withdrawn) The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Gelbvieh cattle is identified.

13. (Withdrawn) The method of claim 1, further comprising marketing the subject prior to harvest based on the inferred breed.

14. (Withdrawn) The method of claim 1, further comprising managing the subject in the feedlot to obtain improved performance based on known characteristics of the inferred breed for the subject.

15. (Withdrawn) The method of claim 1, further comprising identifying a nucleotide sequence of a hypermutable sequence in the sample, and inferring breed based on the at least one nucleotide occurrence and the nucleotide sequence of the hypermutable sequence.

16. (Withdrawn) The method of claim 1, further comprising marketing a product of the bovine subject based on the inferred breed.

17. (Withdrawn) The method of claim 16, wherein the marketing of the product comprises marketing the product under a trademark specific for a breed.

18. (Withdrawn) A method for determining a nucleotide occurrence of a single nucleotide polymorphism (SNP) in a bovine sample, comprising:

a) contacting a bovine polynucleotide in the sample with an oligonucleotide that binds to a target region of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895; and

b) determining the nucleotide occurrence of a single nucleotide polymorphism (SNP) corresponding to position 300 of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the determination comprises analyzing binding of the oligonucleotide, or detecting an amplification product generated using the oligonucleotide, thereby determining the nucleotide occurrence of the SNP.

19. (Withdrawn) The method of claim 18, wherein the oligonucleotide binds to a target sequence that comprises one of the SNPs, and the nucleotide occurrence is determined based on the binding of the oligonucleotide to the target sequence.

20. (Withdrawn) The method of claim 18, wherein the bovine polynucleotide is contacted with a pair of oligonucleotides that comprise a primer pair, and the nucleotide occurrence is determined using an amplification product generated using the primer pair.

21. (Withdrawn) The method of claim 20, wherein at least one primer of the primer pair is any one of SEQ ID NOS:Forward1 to Reverse4868.

22. (Withdrawn) The method of claim 21, wherein the primer pair is any of the forward and reverse primer pairs listed in Table 6.

23. (Withdrawn) The method of claim 19, wherein the terminal nucleotide of the oligonucleotide binds to the SNP.

24. (Withdrawn) The method of claim 23, wherein the method comprises detecting an extension product generated using the oligonucleotide as a primer.

25. (Withdrawn) The method of claim 20, wherein the terminal nucleotide of each oligonucleotide of a pair of oligonucleotides is complementary to a different nucleotide at position 300 of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, or a complement thereof.

26. (Withdrawn) The method of claim 22, wherein the oligonucleotide is any one of SEQ ID NO:4879 to 9736 or SEQ ID NO:64914 to 64922.

27. (Withdrawn) The method of claim 18, wherein the polynucleotide is contacted with a pair of oligonucleotides each comprising a different detectable label.

28. (Canceled)

29. (Currently Amended) An [[The]] isolated polynucleotide ~~of claim 28, wherein the polynucleotide~~ compris[[es]]ing at least 100 contiguous nucleotides of SEQ ID NO[[S]]:4518~~1 to 4868 or SEQ ID NOS:64887 to 64895~~, wherein the polynucleotide is less than or equal to about 500,000 nucleotides in length.

30. (Currently Amended) The isolated polynucleotide of claim 29[[8]], wherein the polynucleotide comprises the polynucleotide sequence of SEQ ID NO:4518 ~~any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895~~.

31. (Currently Amended) The isolated polynucleotide of claim 29, wherein the polynucleotide further comprises a detectable label at a position corresponding to position 300 of SEQ ID NO:4518 ~~any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895~~.

32. (Currently Amended) An isolated oligonucleotide that is complementary to at least 100 contiguous nucleotides of SEQ ID NO:4518 ~~binds to any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the oligonucleotide is at least 10 nucleotides in length~~.

33. (Currently Amended) The oligonucleotide of claim 32, wherein the oligonucleotide comprises a detectable label ~~is any one of SEQ ID NOS:4869 to 19472 or SEQ ID NOS:64896 to 64922~~.

34-36. (Canceled)

37. (Currently Amended) An isolated oligonucleotide comprising 100 contiguous nucleotides, that selectively binds to a target polynucleotide of SEQ ID NO[[S]]:4518 ~~1 to 4868 or SEQ ID NOS:64887 to 64895~~, wherein a terminal nucleotide of the isolated oligonucleotide binds to position 299, 300, or 301 of ~~any one of~~ SEQ ID NO[[S]]:4518 ~~1 to 4868 or SEQ ID NOS:64887 to 64895~~.

38. (Canceled)

39. (Currently Amended) The isolated oligonucleotide of claim 37, wherein the terminal nucleotide binds to position 300 ~~of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895~~.

40. (Currently Amended) The isolated oligonucleotide of claim 37, wherein the oligonucleotide is SEQ ID NO:4518 ~~any one of SEQ ID NO:4879 to 9736 or SEQ ID NO:64914 to 64922~~.

41. (Currently Amended) An isolated vector comprising a polynucleotide of claim 29[[8]].

42. (Previously Presented) An isolated cell comprising the vector of claim 41.

43. (Withdrawn) A method for sorting bovine subjects, comprising:

a) inferring a breed for a first bovine subject from a nucleic acid sample of the first bovine subject, by a method comprising identifying a nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of at least one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the SNP is associated with the breed; and

b) sorting the first bovine subject based on the inferred breed, and repeating for additional subjects, thereby sorting bovine subjects.

44. (Withdrawn) The method of claim 43, wherein the bovine subjects are sorted based on whether they are Angus, Limousin, Brahman, Simmental, Hereford, Gelbvieh or Charolais cattle.

45. (Withdrawn) A method for breeding a bovine subject, comprising:

a) inferring breed of a bovine candidate for use in breeding programs from a nucleic acid sample of the bovine candidate by a method comprising identifying the nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of at least one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the SNP is associated with breed; and

b) determining whether to select the individual for use in breeding programs based on the inferred breed, thereby breeding the bovine subject.

46. (Withdrawn) The method of claim 45, wherein the selection is implemented at the elite or breeding nucleus level or at the multiplier or foundation animal level.

47. (Withdrawn) The method of claim 45, wherein the selected bovine subject is used for breeding.

48. (Withdrawn) A bovine subject resulting from the selection and breeding according to claim 45.

49. (Withdrawn) The method of claim 48, wherein the selected bovine subject is used for cloning.

50. (Withdrawn) A method of providing labeling accuracy for breed identified meat products, comprising:

a) inferring breed of a bovine candidate for use in branded meat products from a nucleic acid sample of the bovine candidate by a method comprising identifying the nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of at least one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the SNP is associated with breed; and

b) determining whether to brand the harvested product based on the inferred breed, thereby providing labeling accuracy for breed identified meat products.

51. (Withdrawn) The method of claim 50, wherein the inferred breed is Angus, Limousin, Brahman, Simmental, Hereford, Gelbvieh or Charolais.

52. (Currently Amended) A kit for determining nucleotide occurrences or haplotype alleles of bovine SNPs, comprising a[[n]] combination of oligonucleotide probe, primer, [[or]] primer pair~~, or combinations thereof,~~ and a container for identifying the nucleotide occurrence of at least one bovine single nucleotide polymorphism (SNP) corresponding to position 300 of SEQ ID NOS:1,

2, 7, 2220, 2248, 2251, 4007, 4501, 4502, 4503, 4518, 64887, and 64888 ~~1 to 4868 or SEQ ID NOS:64887 to 64895~~, wherein the oligonucleotide probe comprises at least 100 contiguous nucleotides of SEQ ID NO:4518, and wherein the SNP is associated with breed.

53. (Previously Presented) The kit of claim 52, further comprising one or more detectable labels.

54. (Currently Amended) The kit of claim 52, wherein the kit comprises a plurality of oligonucleotide probes, primers, and [[or]] primer pairs~~, or combinations thereof~~, for identifying the nucleotide occurrence of at least two of the SNPs.

55. (Currently Amended) The kit of claim 52, wherein the kit comprises at least two probes, primers, and [[or]] primer pairs for identifying the nucleotide occurrence of at least two SNPs that comprise a haplotype, and wherein the kit allows a determination of a haplotype allele that is associated with the trait.

56. (New) A combination of sequences comprising at least SEQ ID NO:4518 and one or more sequences selected from SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:7, SEQ ID NO:2220, SEQ ID NO:2248, SEQ ID NO:2251, SEQ ID NO:4007, SEQ ID NO:4501, SEQ ID NO:4502; SEQ ID NO:4503, SEQ ID NO:64887, or SEQ ID NO:64888, wherein the combination of two or more sequences is predictive of breed determination of greater than about 50% Angus breed.

57 (New) The combination of claim 56, comprising SEQ ID NO:4518 and SEQ ID NO: 64887.

58. (New) The combination of claim 56, comprising SEQ ID NO:4518 and SEQ ID NO:4007.

59. (New) The combination of claim 56, comprising SEQ ID NO:4518 and SEQ ID NO:4501.

60. (New) The combination of claim 56, comprising SEQ ID NO:4518 and SEQ ID NO:64888.

61. (New) The combination of claim 56, comprising SEQ ID NO:4518 and SEQ ID NO:4502.

62. (New) The combination of claim 56, comprising SEQ ID NO:4518 and SEQ ID NO:4503.

63. (New) The combination of claim 56, comprising SEQ ID NO:4518, SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:7, SEQ ID NO:2220, SEQ ID NO:2248, SEQ ID NO:2251, SEQ ID NO:4007, SEQ ID NO:4501, SEQ ID NO:4502; SEQ ID NO:4503, SEQ ID NO:64887, and SEQ ID NO:64888.

64. (New) The combination of claim 56, wherein at least one sequence comprises a detectable label at a position corresponding to position 300.

65. (New) The combination of claim 64, wherein the sequence comprising the detectable is SEQ ID NO:4518.

66. (New) The combination of claim 56, wherein at least one sequence is less than or equal to about 500,000 nucleotides in length.

67. (New) The combination of claim 56, further comprising an oligonucleotide probe, primer, and primer pair corresponding to position 300 of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:7, SEQ ID NO:2220, SEQ ID NO:2248, SEQ ID NO:2251, SEQ ID NO:4007, SEQ ID NO:4501, SEQ ID NO:4502; SEQ ID NO:4503, SEQ ID NO:64887, or SEQ ID NO:64888, wherein the oligonucleotide probe comprises at least 100 contiguous nucleotides of SEQ ID NO:4518, and wherein the SNPs are predictive of breed determination of greater than about 50% of a specific breed.

68. (New) A combination of sequences comprising at least SEQ ID NO:4518 or SEQ ID NO:4502 and one or more sequences selected from SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:7,

SEQ ID NO:2220, SEQ ID NO:2248, SEQ ID NO:2251, SEQ ID NO:4007, SEQ ID NO:4501, SEQ ID NO:4503, SEQ ID NO:64887, SEQ ID NO:64888; SEQ ID NO:4518, when SEQ ID NO:4502 is selected; or SEQ ID NO:4502, when SEQ ID NO:4518 is selected, wherein the combination of two or more sequences is predictive of breed determination of greater than about 50% Angus breed.

69. (New) A combination of two or more isolated nucleic acids comprising at least 100 contiguous nucleotides of the single nucleotide polymorphisms (SNPs) listed in Table 5 or Table 3A, wherein the isolated nucleic acids comprise at least one single nucleotide polymorphism (SNP) corresponding to position 300 of the SNP, and wherein the SNPs are predictive of breed determination.

70. (New) The combination of claim 69, wherein the SNPs are listed in Table 5.

71. (New) The combination of claim 69, wherein the SNPs are listed in Table 3A.

72. (New) The combination of claim 70, comprising the isolated nucleic acid sequences as set forth in SEQ ID NOs: 1-4868 and SEQ ID NOs:64887-64895.

73. (New) The combination of claim 69, wherein at least one isolated nucleic acid comprises SEQ ID NO:4518.

74. (New) The combination of claim 69, wherein at least one isolated nucleic acid further comprises a detectable label at a position corresponding to position 300 of SEQ ID NO:4518.

75. (New) The combination of claim 69, wherein at least one isolated nucleic acid is less than or equal to about 500,000 nucleotides in length.

76. (New) The combination of claim 70, further comprising an oligonucleotide probe, primer, and primer pair corresponding to position 300 of the SNPs listed in Table 5, wherein the oligonucleotide probe comprises at least 100 contiguous nucleotides of SEQ ID NO:4518, and wherein the SNPs are predictive of breed determination of greater than about 50% of a specific breed.